



## SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT OF THE SIGMA-1 RECEPTOR

<130> 9151.6

<140> 09/823,069

<141> 2001-03-30

<150> US 60/193,694

<151> 2000-03-31

<160> 6

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

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gct gtc gca gcg gtg ctg acc cag gtc gtc tgg ctc tgg ctg ggt acg 96  
Ala Val Ala Ala Val Leu Thr Gln Val Val Trp Leu Trp Leu Gly Thr  
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cag agc ttc gtc ttc cag cgc gaa gag ata gcg cag ttg gcg cgg cag 144  
Gln Ser Phe Val Phe Gln Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
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tac gct ggg ctg gac cac gag ctg gcc ttc tct cgt ctg atc gtg gag 192  
Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
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ctg cgg cgg ctg cac cca gcc cac gtg ctg ccc gac gag gag ctg cag 240  
Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
65 70 75 80

tgg gtg ttc gtg aat gcg ggt gcc tgg atg gcc gcc atg tgc ctt ctg 288  
Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu  
85 90 95

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aca gct gtg gag tgg ggg cca aac aca tgg atg gtg gag tac ggc cgg Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg 130 135 140	432
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agc acc cag gac ttc ctc acc ctc ttc tat act ctt cgc tcc tat gct Ser Thr Gln Asp Phe Leu Thr Leu Phe Tyr Thr Leu Arg Ser Tyr Ala 165 170 175	528
cgg ggc ctc cgg ctt gag ctc acc acc tac ctc ttt ggc cag gac cct Arg Gly Leu Arg Leu Glu Leu Thr Thr Tyr Leu Phe Gly Gln Asp Pro 180 185 190	576
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Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu 50 55 60	
Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln 65 70 75 80	
Trp Val Phe Val Asn Ala Gly Gly Trp Met Gly Ala Met Cys Leu Leu 85 90 95	

His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
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Ser Arg Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
 115 120 125

Thr Ala Val Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
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Gly Val Ile Pro Ser Thr Leu Ala Phe Ala Leu Ala Asp Thr Val Phe  
 145 150 155 160

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 Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln  
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 Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu  
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 Leu Arg Arg Leu His Pro Gly His Val Leu Pro Asp Glu Glu Leu Gln  
 65 70 75 80  
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Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg				
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Gly Thr Gln Asp Tyr Leu Thr Leu Phe Tyr Thr Leu Arg Ala Tyr Ala				
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Gln Asn Phe Val Phe Ser Arg Glu Glu Ile Ala Gln Leu Ala Arg Gln				
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Tyr Ala Gly Leu Asp His Glu Leu Ala Phe Ser Arg Leu Ile Val Glu				
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His Ala Ser Leu Ser Glu Tyr Val Leu Leu Phe Gly Thr Ala Leu Gly  
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Ser His Gly His Ser Gly Glu Thr Val Val His Gly Pro Gly Glu Ala  
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Thr Ala Leu Glu Trp Gly Pro Asn Thr Trp Met Val Glu Tyr Gly Arg  
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Gly Val Ile Pro Ser Thr Leu Phe Phe Ala Leu Ala Asp Thr Phe Phe  
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